

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 04:54:30 ; Search time 346.363 Seconds
(without alignments)
8744.444 Million cell updates/sec

8744.444 Million cell updates/sec

Title: US-09-763-011d-1

Perfect score: 1851

Sequence: 1 atgcattatgacattcacc.....tgcttgaataaagtagttg 1851

Scoring table: IDENTITY NTC
Gapop 10.0, Gapept 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 240568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgm2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgm2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgm2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgm2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgm2_6/prodata/1/ina/PCUTS_COMB.seq.*
6: /cgm2_6/prodata/1/ina/backfillseq1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1507.4	81.4	1521	4 US-09-248-796A-5972	Sequence 5972, Ap
2	983.4	53.1	1257	4 US-09-248-796A-5973	Sequence 5973, Ap
3	625.4	33.8	816	4 US-09-248-796A-6065	Sequence 6065, Ap
4	625.2	33.8	1626	4 US-09-614-221A-521	Sequence 521, App
5	544.2	29.4	1704	4 US-09-614-221A-534	Sequence 534, App
6	543.6	29.4	1704	4 US-09-614-221A-96	Sequence 96, App1
7	529.2	28.6	1695	4 US-09-614-221A-443	Sequence 443, App
8	299.4	16.2	417	4 US-09-248-796A-6023	Sequence 6023, App
9	214.4	11.6	243	4 US-09-248-796A-11265	Sequence 11265, A
10	151.2	8.2	2288	4 US-09-248-796A-5965	Sequence 5965, A
11	151	7.8	708	4 US-08-998-416-719	Sequence 719, App
12	144.2	7.8	339	4 US-09-248-796A-5971	Sequence 5971, App
13	124.2	6.7	1662	4 US-09-248-796A-5975	Sequence 5975, Ap
14	80.2	4.3	1125	4 US-09-248-796A-6024	Sequence 6024, Ap
15	72.4	3.9	1960	4 US-09-614-221A-521	Sequence 521, App
16	66.2	3.6	1503	4 US-09-248-796A-5976	Sequence 5976, App
17	64.8	3.5	609	4 US-09-248-796A-6609	Sequence 6609, Ap
18	59.2	3.2	1659	4 US-09-248-796A-6610	Sequence 6610, Ap
19	58	3.1	978	4 US-09-248-796A-5978	Sequence 5978, Ap
20	57	3.1	7218	1 US-08-332-463-14	Sequence 14, App1
21	56.6	3.1	612	4 US-09-802-540-1357	Sequence 1357, Ap
22	54.2	2.9	474	4 US-09-248-796A-149	Sequence 149, App
23	51.4	2.8	5227	4 US-09-919-172-79	Sequence 79, App1
24	51.4	2.8	5228	4 US-09-919-039-216	Sequence 216, App
25	50.6	2.7	597	4 US-09-248-796A-2683	Sequence 2683, Ap
26	50.6	2.7	1089	4 US-09-248-796A-150	Sequence 150, App
27	49.6	2.7	633	4 US-09-248-796A-6030	Sequence 6030, Ap

C	28	49.6	2.7	1039	4 US-09-902-540-1280	Sequence 1280, Ap
C	29	49.4	2.7	405	4 US-09-248-796A-5966	Sequence 5966, Ap
C	30	48.8	2.6	1141	4 US-09-806-708B-22	Sequence 22, App1
C	31	48.8	2.6	1668	4 US-09-614-221A-420	Sequence 420, App
C	32	48.4	2.6	614	4 US-09-902-540-1318	Sequence 1318, Ap
C	33	48.2	2.6	648	4 US-09-248-796A-5974	Sequence 5974, Ap
C	34	48	2.6	429	4 US-09-248-796A-6022	Sequence 6022, Ap
C	35	48	2.6	1137	4 US-09-248-796A-151	Sequence 151, App
C	36	47.8	2.6	1003	4 US-09-134-001C-799	Sequence 799, App
C	37	47.8	2.6	8920	2 US-08-446-855A-1	Sequence 1, App1
C	38	47.8	2.6	8920	3 US-09-150-741-1	Sequence 1, App1
C	39	47.2	2.5	832	4 US-09-621-976-2813	Sequence 2813, Ap
C	40	47	2.5	1141	4 US-09-806-708B-22	Sequence 22, App1
C	41	47	2.5	670689	4 US-09-949-016-12505	Sequence 12505, A
C	42	47	2.5	670690	4 US-09-949-016-14207	Sequence 14207, A
C	43	46.6	2.5	19124	2 US-08-487-826B-13	Sequence 13, App1
C	44	46.2	2.5	828	3 US-08-998-416-538	Sequence 538, App
C	45	46.2	2.5	2672	1 US-08-703-947-1	Sequence 1, App1

ALIGNMENTS

RESULT 1
US-09-248-796A-5972
; Sequence 5972, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5972
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5972

Query Match	81.4%	Score 1507.4;	DB 4;	Length 1521;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1519;	Conservative	0;	Mismatches 1;	Indels 1;
			Gaps	1;
QY	134	AGGAATATATTTGATATGATTTTGTG-TTTCCTATTCCTTTGGTTCGTTT	192	
DB	1	AGGAATATATTTGATATGATTTTGTG-TTTCCTATTCCTTTGGTTCGTTT	60	
QY	193	GGTTTCGATCTGATACCATTTTCGTTTCATTAACATGACTGCTTTTGAAGATT	252	
DB	61	GGTTTCGATCTGATACCATTTTCGTTTCATTAACATGACTGCTTTTGAAGATT	120	
QY	253	GGTGTGATCAAGCTGAGGTGCTCTTACTTTTCAAGTGAAGCTGTTATGATT	312	
DB	121	GGTGTGATCAAGCTGAGGTGCTCTTACTTTTCAAGTGAAGCTGTTATGATT	180	
QY	313	GGTTTTCATGATGGGTTTGGCCATTTGTCATTAATTTTCCAAAGTCGATATG	372	
DB	181	GGTTTTCATGATGGGTTTGGCCATTTGTCATTAATTTTCCAAAGTCGATATG	240	
QY	373	TACGGTGAAGAGTGGTGTGATGATGATGATGATGATGATGATGATGATGAT	432	
DB	241	TACGGTGAAGAGTGGTGTGATGATGATGATGATGATGATGATGATGATGAT	300	
QY	433	CAATATGCTTCAACATGCTTGTATCAATCAATGATGATGATGATGATGATGAT	492	
DB	301	CAATATGCTTCAACATGCTTGTATCAATCAATGATGATGATGATGATGATGAT	360	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:05:29 ; Search time 1231.07 Seconds
(without alignment)
9220.397 Million cell updates/sec

Title: US-09-763-011d-1

Perfect score: 1851
Sequence: 1 atgcatagataattacac.....tgccttgaataatagtttg 1851

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5659437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1645	88.9	1653	18	US-10-451-467A-475
2	1645	88.9	1653	18	US-10-451-467A-579
3	1645	88.9	1653	18	US-10-451-467A-687
4	1645	88.9	1653	18	US-10-451-467A-687
5	1645	88.9	1653	18	US-10-451-467A-477
6	1645	88.9	1653	18	US-10-451-467A-551
7	1645	88.9	1653	18	US-10-369-493-25367
8	1645	88.9	1653	18	US-10-451-467A-121
9	1645	88.9	1653	18	US-10-369-493-25366
10	1645	88.9	1653	18	US-10-451-467A-119
11	1645	88.9	1653	18	US-10-312-783A-3
					US-10-369-493-25368

12	685	37.0	2204	18	US-10-451-467A-123	Sequence 123, App
13	678	36.6	1713	17	US-10-312-783A-4	Sequence 4, Appl
14	662	35.8	1683	17	US-10-369-493-45733	Sequence 45733, A
15	657.2	35.5	1713	17	US-10-369-493-45734	Sequence 45734, A
16	657.2	35.5	2213	18	US-10-451-467A-205	Sequence 205, App
17	625.2	33.8	1626	17	US-10-369-493-25554	Sequence 25554, A
18	625.2	33.8	1626	18	US-10-369-493-25554	Sequence 25554, A
19	625.2	33.8	2126	18	US-10-451-467A-303	Sequence 303, App
20	602.6	32.6	1725	17	US-10-369-493-46000	Sequence 46000, A
21	583.4	31.5	1779	17	US-10-369-493-45735	Sequence 45735, A
22	568.6	30.7	1710	17	US-10-369-493-45814	Sequence 45814, A
23	560.8	30.3	1641	17	US-10-369-493-25695	Sequence 25695, A
24	544.2	29.4	1704	17	US-10-369-493-45814	Sequence 45814, A
25	544.2	29.4	1704	18	US-10-369-493-45812	Sequence 45812, A
26	543.6	29.4	1704	17	US-10-369-493-45812	Sequence 45812, A
27	543.6	29.4	1704	18	US-10-369-493-45812	Sequence 45812, A
28	540.4	29.2	1695	17	US-10-369-493-25693	Sequence 25693, A
29	529.2	28.6	1695	17	US-10-369-493-25693	Sequence 25693, A
30	529.2	28.6	1695	18	US-10-369-493-443	Sequence 443, App
31	509.6	27.5	1704	17	US-10-369-493-25230	Sequence 25230, A
32	506.4	27.4	1704	17	US-10-369-493-45897	Sequence 45897, A
33	473.4	25.6	1374	17	US-10-369-493-45897	Sequence 45897, A
34	334.2	18.1	1605	17	US-10-369-493-25715	Sequence 25715, A
35	326.8	17.7	1593	17	US-10-369-493-46317	Sequence 46317, A
36	319.4	17.3	1638	17	US-10-369-493-46318	Sequence 46318, A
37	260.8	14.1	1668	17	US-10-369-493-26009	Sequence 26009, A
38	254	13.7	1671	17	US-10-369-493-26003	Sequence 26003, A
39	254	13.7	1671	17	US-10-369-493-26009	Sequence 26009, A
40	215.6	11.6	1422	17	US-10-369-493-26158	Sequence 26158, A
41	210.8	11.4	1386	17	US-10-369-493-27920	Sequence 27920, A
42	168.2	9.1	1647	17	US-10-369-493-36063	Sequence 36063, A
43	161	8.7	966	18	US-10-425-115-54539	Sequence 54539, A
44	142.6	7.7	1623	17	US-10-369-493-25623	Sequence 25623, A
45	137.6	7.4	673	18	US-10-653-047-6270	Sequence 6270, App

ALIGNMENTS

RESULT 1
US-10-451-467A-475
Sequence 475, Application US/10451467A
Publication No. US20040161840A1

GENERAL INFORMATION:
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REBKANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10-451,467A
PRIOR FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PatentIn version 3.1
SEQ ID NO 475
LENGTH: 1653
TYPE: DNA
ORGANISM: Candida albicans

US-10-451-467A-475

Query Match 88.9%; Score 1645; DB 18; Length 1653;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ATGTCATTAGTATTTCACAGAAACCGTATTGGAAGAAAGAAATTCAGG 60